



SEQUENCE LISTING

<110> Zoghbi, Huda  
Bellen, Hugo  
Bermingham, Nessim  
Hassan, Bessam  
Ben-Arie, Nissim

<120> Compositions and Methods for Therapeutic Use of Atonal-associated  
Sequence for Deafness, Osteoarthritis, and Abnormal Cell Proliferation

<130> P01899US2

<140> US 09/585,645

<141> 2000-06-01

<150> US 60/137,060

<151> 1999-06-01

<150> US 60/176,993

<151> 2000-01-19

<160> 70

<170> PatentIn version 3.1

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Tyr Pro Pro Glu Leu Ser Leu Leu Asp Ser Thr Asp Pro Arg Ala Trp  
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Leu Ala Pro Thr Leu Gln Gly Ile Cys Thr Ala Arg Ala Ala Gln Tyr  
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Leu Leu His Ser Pro Glu Leu Gly Ala Ser Glu Ala Ala Ala Pro Arg  
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Asp Glu Val Asp Gly Arg Gly Glu Leu Val Arg Arg Ser Ser Gly Gly  
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Ala Ser Ser Ser Lys Ser Pro Gly Pro Val Lys Val Arg Glu Gln Leu  
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Arg Leu Ala Ala Asn Ala Arg Glu Arg Arg Arg Met His Gly Leu Asn  
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His Ala Phe Asp Gln Leu Arg Asn Val Ile Pro Ser Phe Asn Asn Asp  
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Lys Lys Leu Ser Lys Tyr Glu Thr Leu Gln Met Ala Gln Ile Tyr Ile  
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Asn Ala Leu Ser Glu Leu Leu Gln Thr Pro Ser Gly Gly Glu Gln Pro  
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Pro Pro Pro Pro Ala Ser Cys Lys Ser Asp His His His Leu Arg Thr  
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Ala Ala Ser Tyr Glu Gly Gly Ala Gly Asn Ala Thr Ala Ala Gly Ala  
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Arg Thr Arg Phe Ser Ala Pro Ala Ser Ala Gly Gly Tyr Ser Val Gln  
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Leu Asp Ala Leu His Phe Ser Thr Phe Glu Asp Ser Ala Leu Thr Ala  
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Met Met Ala Gln Lys Asn Leu Ser Pro Ser Leu Pro Gly Ser Ile Leu  
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Arg Gly Gly Arg Asn Arg Pro Lys Ser Glu Leu Ala Leu Ser Lys Gln  
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Arg Arg Ser Arg Arg Lys Lys Ala Asn Asp Arg Glu Arg Asn Arg Met  
85 90 95

His Asn Leu Asn Ser Ala Leu Asp Ala Leu Arg Gly Val Leu Pro Thr  
100 105 110

Phe Pro Asp Asp Ala Lys Leu Thr Lys Ile Glu Thr Leu Arg Phe Ala  
115 120 125

His Asn Tyr Ile Trp Ala Leu Thr Gln Thr Leu Arg Ile Ala Asp His  
130 135 140

Ser Phe Tyr Gly Pro Glu Pro Pro Val Pro Cys Gly Glu Leu Gly Ser  
145 150 155 160

Pro Gly Gly Gly Ser Asn Gly Asp Trp Gly Ser Ile Tyr Ser Pro Val  
165 170 175

Ser Gln Ala Gly Asn Leu Ser Pro Thr Ala Ser Leu Glu Glu Phe Pro  
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Val Phe Ser Asp Phe Leu  
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Asp Ala Lys Leu Thr Lys Ile Glu Thr Leu Arg Phe Ala His Asn Tyr  
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Ile Trp Ala Leu Thr Glu Thr Leu Arg Leu Ala Asp His Cys Ala Gly  
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Ala Gly Gly Leu Gln Gly Ala Leu Phe Thr Glu Ala Val Leu Leu Ser  
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Pro Gly Ala Ala Leu Gly Ala Ser Gly Asp Ser Pro Ser Pro Pro Ser  
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Ser Trp Ser Cys Thr Asn Ser Pro Ala Ser Ser Ser Asn Ser Thr Ser  
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Pro Tyr Ser Cys Thr Leu Ser Pro Ala Ser Pro Gly Ser Asp Val Asp  
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Lys Arg Ala Pro Gly Glu Glu Thr Glu Lys Glu Glu Glu Glu Asp  
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Arg Glu Glu Glu Asp Glu Asn Gly Leu Ser Arg Arg Arg Gly Leu Arg  
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Lys Lys Lys Thr Thr Lys Leu Arg Leu Glu Arg Val Lys Phe Arg Arg  
85 90 95

Gln Glu Ala Asn Ala Arg Glu Arg Asn Arg Met His Gly Leu Asn Asp  
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Ala Leu Asp Asn Leu Arg Lys Val Val Pro Cys Tyr Ser Lys Thr Gln  
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Lys Leu Ser Lys Ile Glu Thr Leu Arg Leu Ala Lys Asn Tyr Ile Trp  
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Ala Leu Ser Glu Ile Leu Arg Ile Gly Lys Arg Pro Asp Leu Leu Thr  
145 150 155 160

Phe Val Gln Asn Leu Cys Lys Gly Leu Ser Gln Pro Thr Thr Asn Leu  
165 170 175

Val Ala Gly Cys Leu Gln Leu Asn Ala Arg Ser Phe Leu Met Gly Gln  
180 185 190

Gly Gly Glu Ala Ala His His Thr Arg Ser Pro Tyr Ser Thr Phe Tyr  
195 200 205

Pro Pro Tyr His Ser Pro Glu Leu Ala Thr Pro Pro Gly His Gly Thr  
210 215 220

Leu Asp Asn Ser Lys Ser Met Lys Pro Tyr Asn Tyr Cys Ser Ala Tyr  
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Glu Ser Phe Tyr Glu Ser Thr Ser Pro Glu Cys Ala Ser Pro Gln Phe  
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Glu Gly Pro Leu Ser Pro Pro Pro Ile Asn Tyr Asn Gly Ile Phe Ser  
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Leu Lys Gln Glu Glu Thr Leu Asp Tyr Gly Lys Asn Tyr Asn Tyr Gly  
 275 280 285

Met His Tyr Cys Ala Val Pro Pro Arg Gly Pro Leu Gly Gln Gly Ala  
 290 295 300

Met Phe Arg Leu Pro Thr Asp Ser His Phe Pro Tyr Asp Leu His Leu  
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Ala Glu Leu Ser Leu Leu Asp Ser Thr Asp Pro Arg Ala Trp Leu Thr  
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Pro Thr Leu Gln Gly Leu Cys Thr Ala Arg Ala Ala Gln Tyr Leu Leu  
 65 70 75 80

His Ser Pro Glu Leu Gly Ala Ser Glu Ala Ala Ala Pro Arg Asp Glu  
 85 90 95

Ala Asp Ser Gln Gly Glu Leu Val Arg Arg Ser Gly Cys Gly Gly Leu  
 100 105 110

Ser Lys Ser Pro Gly Pro Val Lys Val Arg Glu Gln Leu Cys Lys Leu  
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Lys Gly Gly Val Val Val Asp Glu Leu Gly Cys Ser Arg Gln Arg Ala  
 130 135 140

Pro Ser Ser Lys Gln Val Asn Gly Val Gln Lys Gln Arg Arg Leu Ala  
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Ala Asn Ala Arg Glu Arg Arg Arg Met His Gly Leu Asn His Ala Phe  
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Asp Gln Leu Arg Asn Val Ile Pro Ser Phe Asn Asn Asp Lys Lys Leu  
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Ser Lys Tyr Glu Thr Leu Gln Met Ala Gln Ile Tyr Ile Asn Ala Leu  
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Phe Ser Gly Pro Ala Ser Ser Gly Gly Tyr Ser Val Gln Leu Asp Ala  
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35 40 45

Leu Asp Ala Ala Gly Gly Thr Gln Thr Glu Leu Gly Pro Ile Met Glu  
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Val Gln Gly Gln His Thr Gln Pro Gln Thr Lys Arg Arg Ser Asn Ser  
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Ser Thr Gly Ser Asp Gly Arg Lys Ser Ser Pro Glu Gln Thr Asn Leu  
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Ser Pro Thr Val Gln Lys Arg Arg Arg Gln Ala Ala Asn Ala Arg Glu  
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Arg Lys Arg Met Asn Gly Leu Asn Ala Ala Phe Glu Arg Leu Arg Glu  
115 120 125

Val Val Pro Ala Pro Ser Ile Asp Gln Lys Leu Ser Lys Phe Glu Thr  
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Leu Gln Met Ala Gln Ser Tyr Ile Leu Ala Leu Cys Asp Leu Leu Asn  
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Asn Gly Asp Val Glu Val Asp Ala Ala Ala Tyr Thr Ile Phe Gly Asp  
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 <212> PRT  
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<400> 19

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25

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Glu Ala Leu Leu His Thr Leu Lys Arg Ser Arg Arg Val Lys Ala Asn  
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Asp Arg Glu Arg Asn Arg Met His His Leu Asn Ala Ala Leu Asp Glu  
 50 55 60

Leu Arg Ser Val Leu Pro Thr Phe Pro Asp Asp Thr Lys Leu Thr Lys  
 65 70 75 80

Ile Glu Thr Leu Arg Phe Ala Tyr Asn Tyr Ile Trp Ala Leu Ser Glu  
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Thr Leu Arg Leu Ala Glu Gln Cys Leu Pro Pro Pro Pro Ala Phe Arg  
 100 105 110

Gly Pro Pro Ala Pro Pro Ser Pro Gly Ser Asp Ala Gly Ser Trp Leu  
 115 120 125

Ser Ser Gly Ser Pro Ala Ala Pro Ser Leu Cys Ala Ser Ala Ser Gly  
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Pro Ser Ser Pro Ala Thr Ser Glu Asp Cys Gly Tyr Val Pro Ser Asp  
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Cys Arg

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 35 40 45

Leu Gln Glu Gly Ala Arg Arg Ala Gly Arg Gln Arg Gly Pro Pro Arg  
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Ala Ala Arg Thr Ala Glu Thr Ala Gln Arg Ile Lys Arg Ser Arg Arg  
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Leu Lys Ala Asn Asn Arg Glu Arg Asn Arg Met His Asn Leu Asn Ala  
 85 90 95

Ala Leu Asp Ala Leu Arg Asp Val Leu Pro Thr Phe Pro Glu Asp Ala  
 100 105 110

Lys Leu Thr Lys Ile Glu Thr Leu Arg Phe Ala His Asn Tyr Ile Trp  
 115 120 125

Ala Leu Thr Glu Thr Leu Arg Leu Ala Gly Ala Ala Arg Leu Gly Gly  
 130 135 140

Ala Ala Asp Ala Ala Pro Gly Ala Ala Ala Glu Gly Ser Pro Ser Pro



Arg Glu Arg Arg Arg Met Gln Gly Leu Asn Thr Ala Phe Asp Arg Leu  
50 55 60

Arg Arg Val Val Pro Gln Trp Gly Gln Asp Lys Lys Leu Ser Lys Tyr  
65 70 75 80

Glu Thr Leu Gln Met Ala Leu Ser Tyr Ile Ile Ala Leu Thr Arg Ile  
85 90 95

Leu Ala Glu Ala Glu Arg Asp Trp Val Gly Leu Arg Cys Glu Gln Arg  
100 105 110

Gly Arg Asp His Pro Tyr Leu Pro Phe Pro Gly Ala Arg Leu Gln Val  
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20 25 30

Asn Ser Thr Pro Pro Ser Pro Thr Leu Ile Pro Arg Asp Cys Ser Glu  
35 40 45

Ala Glu Val Gly Asp Cys Arg Gly Thr Ser Arg Lys Leu Arg Ala Arg  
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Arg Gly Gly Arg Asn Arg Pro Lys Ser Glu Leu Ala Leu Ser Lys Gln  
65 70 75 80

Arg Arg Ser Arg Arg Lys Lys Ala Asn Asp Arg Glu Arg Asn Arg Met  
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His Asn Leu Asn Ser Ala Leu Asp Ala Leu Arg Gly Val Leu Pro Thr  
100 105 110

Phe Pro Asp Asp Ala Lys Leu Thr Lys Ile Glu Thr Leu Arg Phe Ala  
115 120 125

His Asn Tyr Ile Trp Ala Leu Thr Gln Thr Leu Arg Ile Ala Asp His  
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Ser Phe Tyr Gly Pro Glu Pro Pro Val Pro Cys Gly Glu Leu Gly Ser  
145 150 155 160

Pro Gly Gly Gly Ser Asn Gly Asp Trp Gly Ser Ile Tyr Ser Pro Val  
165 170 175

Ser Gln Ala Gly Asn Leu Ser Pro Thr Ala Ser Leu Glu Glu Phe Pro  
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Gly Leu Gln Val Pro Ser Ser Pro Ser Tyr Leu Leu Pro Gly Ala Leu  
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Val Phe Ser Asp Phe Leu  
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<212> PRT  
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Cys Tyr Ser Lys Thr Gln Lys Leu  
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<212> DNA  
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<211> 263

<212> PRT

<213> MOUSE

<400> 31

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 Ser Arg Gly Ala Lys Thr Ala Glu Thr Val Gln Arg Ile Lys Lys Thr  
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 Arg Arg Leu Lys Ala Asn Asn Arg Glu Arg Asn Arg Met His Asn Leu  
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 Asn Ala Ala Leu Asp Ala Leu Arg Glu Val Leu Pro Thr Phe Pro Glu  
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 Asp Ala Lys Leu Thr Lys Ile Glu Thr Leu Arg Phe Ala His Asn Tyr  
 145 150 155 160  
 Ile Trp Ala Leu Thr Glu Thr Leu Arg Leu Ala Asp His Cys Ala Gly  
 165 170 175  
 Ala Gly Gly Leu Gln Gly Ala Leu Phe Thr Glu Ala Val Leu Leu Ser  
 180 185 190  
 Pro Gly Ala Ala Leu Gly Ala Ser Gly Asp Ser Pro Ser Pro Pro Ser  
 195 200 205  
 Ser Trp Ser Cys Thr Asn Ser Pro Ala Ser Ser Ser Asn Ser Thr Ser  
 210 215 220  
 Pro Tyr Ser Cys Thr Leu Ser Pro Ala Ser Pro Gly Ser Asp Val Asp  
 225 230 235 240  
 Tyr Trp Gln Pro Pro Pro Pro Glu Lys His Arg Tyr Ala Pro His Leu  
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Pro Leu Ala Arg Asp Cys Ile  
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<212> DNA  
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<210> 33  
 <211> 330  
 <212> PRT  
 <213> MOUSE

<400> 33

Met Ala Lys Met Tyr Met Lys Ser Lys Asp Met Val Glu Leu Val Asn  
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Thr Gln Ser Trp Met Asp Lys Gly Leu Ser Ser Gln Asn Glu Met Lys  
 20 25 30

Glu Gln Glu Arg Arg Pro Gly Ser Tyr Gly Met Leu Gly Thr Leu Thr  
 35 40 45

Glu Glu His Asp Ser Ile Glu Glu Asp Glu Glu Glu Glu Glu Asp Gly  
 50 55 60

Asp Lys Pro Lys Arg Arg Gly Pro Lys Lys Lys Lys Met Thr Lys Ala  
 65 70 75 80

Arg Leu Glu Arg Phe Arg Ala Arg Arg Val Lys Ala Asn Ala Arg Glu  
 85 90 95

Arg Thr Arg Met His Gly Leu Asn Asp Ala Leu Asp Asn Leu Arg Arg  
 100 105 110

Val Met Pro Cys Tyr Ser Lys Thr Gln Lys Leu Ser Lys Ile Glu Thr  
 115 120 125

Leu Arg Leu Ala Arg Asn Tyr Ile Trp Ala Leu Ser Glu Val Leu Glu  
 130 135 140

Thr Gly Gln Thr Leu Glu Gly Lys Gly Phe Val Glu Met Leu Cys Lys  
 145 150 155 160

Gly Leu Ser Gln Pro Thr Ser Asn Leu Val Ala Gly Cys Leu Gln Leu  
 165 170 175

Gly Pro Gln Ser Thr Leu Leu Glu Lys His Glu Glu Lys Ser Ser Ile  
 180 185 190

Cys Asp Ser Thr Ile Ser Val His Ser Phe Asn Tyr Gln Ser Pro Gly  
 195 200 205

Leu Pro Ser Pro Pro Tyr Gly His Met Glu Thr His Ser Leu His Leu  
 210 215 220

Lys Pro Gln Pro Phe Lys Ser Leu Gly Asp Ser Phe Gly Ser His Pro  
 225 230 235 240

Pro Asp Cys Ser Thr Pro Pro Tyr Glu Gly Pro Leu Thr Pro Pro Leu  
 245 250 255

Ser Ile Ser Gly Asn Phe Ser Leu Lys Gln Asp Gly Ser Pro Asp Leu  
 260 265 270

Glu Lys Ser Tyr Asn Phe Met Pro His Tyr Thr Ser Ala Ser Leu Ser  
 275 280 285

Ser Gly His Val His Ser Thr Pro Phe Gln Thr Gly Thr Pro Arg Tyr  
 290 295 300

Asp Val Pro Val Asp Leu Ser Tyr Asp Ser Tyr Ser His His Ser Ile  
 305 310 315 320

Gly Thr Gln Leu Asn Thr Ile Phe Ser Asp  
 325 330

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 <211> 800  
 <212> DNA  
 <213> MOUSE

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 aagtcttttc agttccctta gttttcaccc atcaacttca gcagcccaca ccctctagtt 240  
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 cttgtgaagg aggtgtgtct ttaggctagg aaggggaggg gctaccctgt gggcaacatc 360  
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 <211> 515  
 <212> DNA  
 <213> CHICKEN

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<210> 36  
 <211> 151  
 <212> PRT  
 <213> CHICKEN

<400> 36

Met Lys Thr Cys Gln Ser Ser His Leu Asp Ser Gly Val Glu Ser Asp  
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Ile Gln Cys Arg Ser Gly Ser Gly Cys Val Val Lys Cys Ser Thr Glu  
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Arg Met Glu Ser Ala Ala Lys Arg Arg Leu Ala Ala Asn Ala Arg Glu  
 35 40 45

Arg Arg Arg Met Gln Gly Leu Asn Thr Ala Phe Asp Arg Leu Arg Lys  
 50 55 60

Val Val Pro Gln Trp Gly Gln Asp Lys Lys Leu Ser Lys Tyr Glu Thr  
65 70 75 80

Leu Gln Met Ala Leu Ser Tyr Ile Met Ala Leu Thr Arg Ile Leu Ala  
85 90 95

Glu Ala Glu Arg Tyr Ser Thr Glu Arg Glu Trp Ile Asn Leu His Cys  
100 105 110

Glu His Phe His Pro Glu Ser Tyr His His Tyr Thr Gly Gln Lys Val  
115 120 125

Ala Thr Asp Ser Asp Pro Tyr Ala Gln Arg Ile Phe Ser Tyr His Pro  
130 135 140

Glu His Phe Gln Ile Ala Asn  
145 150

<210> 37  
<211> 1412  
<212> DNA  
<213> MOUSE

<400> 37  
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gaagaggagg tactgatgct gctgggctcg gcttccccgg cctcggcgac cctgaccccg 180  
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<210> 38  
 <211> 263  
 <212> PRT  
 <213> MOUSE

<400> 38

Met Phe Val Lys Ser Glu Thr Leu Glu Leu Lys Glu Glu Glu Glu Val  
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Leu Met Leu Leu Gly Ser Ala Ser Pro Ala Ser Ala Thr Leu Thr Pro  
 20 25 30

Met Ser Ser Ser Ala Asp Glu Glu Glu Asp Glu Glu Leu Arg Arg Pro  
 35 40 45

Gly Ser Ala Arg Gly Gln Arg Gly Ala Glu Ala Gly Gln Gly Val Gln  
 50 55 60

Gly Ser Pro Ala Ser Gly Ala Gly Gly Cys Arg Pro Gly Arg Leu Leu  
 65 70 75 80

Gly Leu Met His Glu Cys Lys Arg Arg Pro Ser Arg Ser Arg Ala Val  
 85 90 95

Ser Arg Gly Ala Lys Thr Ala Glu Thr Val Gln Arg Ile Lys Lys Thr  
 100 105 110

Arg Arg Leu Lys Ala Asn Asn Arg Glu Arg Asn Arg Met His Asn Leu  
 115 120 125

Asn Ala Ala Leu Asp Ala Leu Arg Glu Val Leu Pro Thr Phe Pro Glu  
 130 135 140

Asp Ala Lys Leu Thr Lys Ile Glu Thr Leu Arg Phe Ala His Asn Tyr  
 145 150 155 160

Ile Trp Ala Leu Thr Glu Thr Leu Arg Leu Ala Asp His Cys Ala Gly  
 165 170 175

Ala Gly Gly Leu Gln Gly Ala Leu Phe Thr Glu Ala Val Leu Leu Ser  
 180 185 190

Pro Gly Ala Ala Leu Gly Ala Ser Gly Asp Ser Pro Ser Pro Pro Ser  
 195 200 205

Ser Trp Ser Cys Thr Asn Ser Pro Ala Ser Ser Ser Asn Ser Thr Ser  
 210 215 220

Pro Tyr Ser Cys Thr Leu Ser Pro Ala Ser Pro Gly Ser Asp Val Asp  
 225 230 235 240

Tyr Trp Gln Pro Pro Pro Pro Glu Lys His Arg Tyr Ala Pro His Leu  
 245 250 255

Pro Leu Ala Arg Asp Cys Ile  
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<210> 39  
 <211> 938  
 <212> DNA  
 <213> ZEBRA FISH

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 gaatggatgg aatgagcacg gatacaagag aggtggttga actcgacgtc cagcattcga 180  
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aagccgaccc gccaaactgc gacctgctgc atgccaacgt gttagaaacg gaccgatctc 720  
ccagaggatc accggggcgtc tgtcggagag gcacggggcgt gggttacccg taccagtacg 780  
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tcgcctcact gaagtgcgag tgagacctgc ccgggcgg 938

<210> 40  
<211> 266  
<212> PRT  
<213> ZEBRA FISH

<400> 40

Met Asp Gly Met Ser Thr Asp Thr Arg Glu Val Val Glu Leu Asp Val  
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Gln His Ser Ser Leu Gly Arg Gly Glu Gln Ser Lys Tyr Pro Pro Ala  
20 25 30

Leu Ala Leu Met Ala Ser Ser Asp Pro Arg Ala Trp Leu Ala Pro Val  
35 40 45

Gln Ala Gly Thr Cys Ala Ala His Ala Glu Tyr Leu Leu His Ser Pro  
50 55 60

Gly Ser Ser Ala Glu Gly Val Ser Ser Ala Ser Asn Phe Arg Lys Ser  
65 70 75 80

Ser Lys Ser Pro Val Lys Val Arg Glu Leu Cys Arg Leu Lys Gly Ala  
85 90 95

Val Gly Ala Asp Glu Gly Arg Gln Arg Ala Pro Ser Ser Lys Ser Thr  
100 105 110

Asn Val Val Gln Lys Gln Arg Arg Met Ala Ala Asn Ala Arg Glu Arg  
115 120 125

Arg Arg Met His Gly Leu Asn His Ala Phe Asp Glu Leu Arg Ser Val  
130 135 140

Ile Pro Ala Phe Asp Asn Asp Lys Lys Leu Ser Lys Tyr Glu Thr Leu  
145 150 155 160

Gln Met Ala Gln Ile Tyr Ile Asn Ala Leu Ser Asp Leu Leu Gln Gly  
165 170 175

Pro Gly Ala Lys Ala Asp Pro Pro Asn Cys Asp Leu Leu His Ala Asn  
 180 185 190

Val Leu Glu Thr Asp Arg Ser Pro Arg Gly Ser Pro Gly Val Cys Arg  
 195 200 205

Arg Gly Thr Gly Val Gly Tyr Pro Tyr Gln Tyr Glu Asp Gly Thr Phe  
 210 215 220

Asn Ser Phe Met Glu Gln Asp Leu Gln Ser Pro Ser Gly Thr Ser Lys  
 225 230 235 240

Ser Gly Ser Glu Ala Ser Lys Asp Ser Pro Arg Ser Asn Arg Ser Asp  
 245 250 255

Gly Glu Val Leu Ala Ser Leu Lys Cys Glu  
 260 265

<210> 41  
 <211> 948  
 <212> DNA  
 <213> FROG

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 ggcagcattg atggagaaga ggatgatgaa gaagaagagg atggagagaa accaaaaaag 180  
 aggggaccca aaaaaaagaa gatgaccaag gctagagtgg agagggtccg tgtccgtaga 240  
 gtaaaagcca atgccaggga gcgttcaaga atgcatggac ttaatgatgc cctggaaaat 300  
 ttgagaaggg ttatgccttg ctattccaaa acacaaaagt tgtctaaaat tgagactctt 360  
 agactggcca gaaactatat atgggcatta tctgatattc tagaacaagg tcaaaatgca 420  
 gagggaaagg gctttctgga aatactctgc aaagggtcttt ctcagccaac aagcaactta 480  
 gtagctggct gcttgcaact tggacctcag gccatgttct tggataaaca cgaagaaaag 540  
 tctcatatat gtgattcctc tcttactggc catacttata attaccagtc cccaggacta 600  
 cccagtcctc cttatggtaa cattgatgtt caccacttgc acttgaaacc ctcttctttc 660  
 aaaccagtaa tggatccttc tgtggtaacc catacactta actgtaccac tccaccatat 720  
 gaaggagctc taacacctcc actcagcatc ggtggtaatt tttctttgaa gcaagatagt 780  
 tcacccgata tggataaatc atatgcattc aggtccccct atccagctct tgggcttggt 840  
 ggatctcatg gacatgcgtc acactttcat accagtgttc caaggatatga actaccata 900

gacatggctt acgagcctta cccacaccat gctatatattca ctgaataa

948

<210> 42  
<211> 315  
<212> PRT  
<213> FROG

<400> 42

Met Ser Glu Met Val Asn Val His Gly Trp Met Glu Glu Ala Leu Ser  
1 5 10 15

Ser Gln Asp Glu Met Lys Glu Arg Asn Gln Ser Ala Tyr Asp Ile Ile  
20 25 30

Ser Gly Leu Cys His Glu Glu Arg Gly Ser Ile Asp Gly Glu Glu Asp  
35 40 45

Asp Glu Glu Glu Glu Asp Gly Glu Lys Pro Lys Lys Arg Gly Pro Lys  
50 55 60

Lys Lys Lys Met Thr Lys Ala Arg Val Glu Arg Phe Arg Val Arg Arg  
65 70 75 80

Val Lys Ala Asn Ala Arg Glu Arg Ser Arg Met His Gly Leu Asn Asp  
85 90 95

Ala Leu Glu Asn Leu Arg Arg Val Met Pro Cys Tyr Ser Lys Thr Gln  
100 105 110

Lys Leu Ser Lys Ile Glu Thr Leu Arg Leu Ala Arg Asn Tyr Ile Trp  
115 120 125

Ala Leu Ser Asp Ile Leu Glu Gln Gly Gln Asn Ala Glu Gly Lys Gly  
130 135 140

Phe Leu Glu Ile Leu Cys Lys Gly Leu Ser Gln Pro Thr Ser Asn Leu  
145 150 155 160

Val Ala Gly Cys Leu Gln Leu Gly Pro Gln Ala Met Phe Leu Asp Lys  
165 170 175

His Glu Glu Lys Ser His Ile Cys Asp Ser Ser Leu Thr Gly His Thr  
180 185 190

Tyr Asn Tyr Gln Ser Pro Gly Leu Pro Ser Pro Pro Tyr Gly Asn Ile  
195 200 205

Asp Val His His Leu His Leu Lys Pro Ser Ser Phe Lys Pro Val Met  
 210 215 220

Asp Pro Ser Val Val Thr His Thr Leu Asn Cys Thr Thr Pro Pro Tyr  
 225 230 235 240

Glu Gly Ala Leu Thr Pro Pro Leu Ser Ile Gly Gly Asn Phe Ser Leu  
 245 250 255

Lys Gln Asp Ser Ser Pro Asp Met Asp Lys Ser Tyr Ala Phe Arg Ser  
 260 265 270

Pro Tyr Pro Ala Leu Gly Leu Gly Gly Ser His Gly His Ala Ser His  
 275 280 285

Phe His Thr Ser Val Pro Arg Tyr Glu Leu Pro Ile Asp Met Ala Tyr  
 290 295 300

Glu Pro Tyr Pro His His Ala Ile Phe Thr Glu  
 305 310 315

<210> 43  
 <211> 1550  
 <212> DNA  
 <213> MOUSE

<400> 43  
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 caatgtgagg accagaaaca aattaagaaa ccagagagct ttccaaaaca agttgtcctt 180  
 cgaggaaaga gcattaaaag ggcccctgga gaagaaaccg agaaagaaga ggaggaagaa 240  
 gacagagagg aagaagatga gaatggcttg tccagaagga gggggctcag gaaaaaaaaag 300  
 accaccaaac tacgactgga aaggggtcaag ttcaggagac aggaagctaa tgcgcgcgag 360  
 aggaaccgga tgcacggcct caatgatgct ctggacaatt tgcgaaaagt ggtcccctgt 420  
 tactctaaaa cccaaaaaact gtccaaaata gaaactttac gactggccaa aaattacatc 480  
 tgggcacttt ctgaaattct gaggattggc aagagaccgg atctgctcac gttcgtccaa 540  
 aacttatgca aaggtctttc ccagccaact acaaacttgg tggcaggctg cttacagctc 600  
 aacgccagaa gtttcctgat gggtcagggt ggggaggctg cccaccacac aaggtcaccc 660  
 tactccacat tctaccacc ctaccacagc cctgagctgg ccactcccc agggcatggg 720  
 actcttgata attccaagtc catgaaacc tacaattact gcagtgcata tgaatccttc 780

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aattacaatt atggcatgca ttactgtgca gtgccacca ggggtccctt tgggcagggt      960
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<210> 44
<211> 337
<212> PRT
<213> MOUSE

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<400> 44

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Met Cys Arg Lys Phe Ala Arg Gln Cys Glu Asp Gln Lys Gln Ile Lys
          20           25           30

```

```

Lys Pro Glu Ser Phe Pro Lys Gln Val Val Leu Arg Gly Lys Ser Ile
          35           40           45

```

```

Lys Arg Ala Pro Gly Glu Glu Thr Glu Lys Glu Glu Glu Glu Asp
          50           55           60

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```

Arg Glu Glu Glu Asp Glu Asn Gly Leu Ser Arg Arg Arg Gly Leu Arg
65           70           75           80

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```

Lys Lys Lys Thr Thr Lys Leu Arg Leu Glu Arg Val Lys Phe Arg Arg
          85           90           95

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Gln Glu Ala Asn Ala Arg Glu Arg Asn Arg Met His Gly Leu Asn Asp
          100          105          110

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Ala Leu Asp Asn Leu Arg Lys Val Val Pro Cys Tyr Ser Lys Thr Gln  
115 120 125

Lys Leu Ser Lys Ile Glu Thr Leu Arg Leu Ala Lys Asn Tyr Ile Trp  
130 135 140

Ala Leu Ser Glu Ile Leu Arg Ile Gly Lys Arg Pro Asp Leu Leu Thr  
145 150 155 160

Phe Val Gln Asn Leu Cys Lys Gly Leu Ser Gln Pro Thr Thr Asn Leu  
165 170 175

Val Ala Gly Cys Leu Gln Leu Asn Ala Arg Ser Phe Leu Met Gly Gln  
180 185 190

Gly Gly Glu Ala Ala His His Thr Arg Ser Pro Tyr Ser Thr Phe Tyr  
195 200 205

Pro Pro Tyr His Ser Pro Glu Leu Ala Thr Pro Pro Gly His Gly Thr  
210 215 220

Leu Asp Asn Ser Lys Ser Met Lys Pro Tyr Asn Tyr Cys Ser Ala Tyr  
225 230 235 240

Glu Ser Phe Tyr Glu Ser Thr Ser Pro Glu Cys Ala Ser Pro Gln Phe  
245 250 255

Glu Gly Pro Leu Ser Pro Pro Pro Ile Asn Tyr Asn Gly Ile Phe Ser  
260 265 270

Leu Lys Gln Glu Glu Thr Leu Asp Tyr Gly Lys Asn Tyr Asn Tyr Gly  
275 280 285

Met His Tyr Cys Ala Val Pro Pro Arg Gly Pro Leu Gly Gln Gly Ala  
290 295 300

Met Phe Arg Leu Pro Thr Asp Ser His Phe Pro Tyr Asp Leu His Leu  
305 310 315 320

Arg Ser Gln Ser Leu Thr Met Gln Asp Glu Leu Asn Ala Val Phe His  
325 330 335

Asn



<210> 45  
 <211> 1393  
 <212> DNA  
 <213> MOUSE

<400> 45  
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 ctgctaccct gcaggcgaga gaccttcccg tctaccggc agaactgtcc ctctggata 360  
 gcaccgaccc acgcgcctgg ctgactccca ctttgcaggg cctctgcacg gcacgcgccg 420  
 cccagtatat gctgcattct cccgagctgg gtgcctccga ggccgcggcg cccggggacg 480  
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<210> 46  
 <211> 351  
 <212> PRT  
 <213> MOUSE

<400> 46

Met Ser Arg Leu Leu His Ala Glu Glu Trp Ala Glu Val Lys Glu Leu  
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 Gly Asp His His Arg His Pro Gln Pro His His Val Pro Pro Leu Thr  
 20 25 30  
 Pro Gln Pro Pro Ala Thr Leu Gln Ala Arg Asp Leu Pro Val Tyr Pro  
 35 40 45  
 Ala Glu Leu Ser Leu Leu Asp Ser Thr Asp Pro Arg Ala Trp Leu Thr  
 50 55 60  
 Pro Thr Leu Gln Gly Leu Cys Thr Ala Arg Ala Ala Gln Tyr Leu Leu  
 65 70 75 80  
 His Ser Pro Glu Leu Gly Ala Ser Glu Ala Ala Ala Pro Arg Asp Glu  
 85 90 95  
 Ala Asp Ser Gln Gly Glu Leu Val Arg Arg Ser Gly Cys Gly Gly Leu  
 100 105 110  
 Ser Lys Ser Pro Gly Pro Val Lys Val Arg Glu Gln Leu Cys Lys Leu  
 115 120 125  
 Lys Gly Gly Val Val Val Asp Glu Leu Gly Cys Ser Arg Gln Arg Ala  
 130 135 140  
 Pro Ser Ser Lys Gln Val Asn Gly Val Gln Lys Gln Arg Arg Leu Ala  
 145 150 155 160  
 Ala Asn Ala Arg Glu Arg Arg Arg Met His Gly Leu Asn His Ala Phe  
 165 170 175  
 Asp Gln Leu Arg Asn Val Ile Pro Ser Phe Asn Asn Asp Lys Lys Leu  
 180 185 190  
 Ser Lys Tyr Glu Thr Leu Gln Met Ala Gln Ile Tyr Ile Asn Ala Leu  
 195 200 205  
 Ser Glu Leu Leu Gln Thr Pro Asn Val Gly Glu Gln Pro Pro Pro Pro  
 210 215 220  
 Thr Ala Ser Cys Lys Asn Asp His His His Leu Arg Thr Ala Ser Ser  
 225 230 235 240

Tyr Glu Gly Gly Ala Gly Ala Ser Ala Val Ala Gly Ala Gln Pro Ala  
245 250 255

Pro Gly Gly Gly Pro Arg Pro Thr Pro Pro Gly Pro Cys Arg Thr Arg  
260 265 270

Phe Ser Gly Pro Ala Ser Ser Gly Gly Tyr Ser Val Gln Leu Asp Ala  
275 280 285

Leu His Phe Pro Ala Phe Glu Asp Arg Ala Leu Thr Ala Met Met Ala  
290 295 300

Gln Lys Asp Leu Ser Pro Ser Leu Pro Gly Gly Ile Leu Gln Pro Val  
305 310 315 320

Gln Glu Asp Asn Ser Lys Thr Ser Pro Arg Ser His Arg Ser Asp Gly  
325 330 335

Glu Phe Ser Pro His Ser His Tyr Ser Asp Ser Asp Glu Ala Ser  
340 345 350

<210> 47  
<211> 993  
<212> DNA  
<213> MOUSE

<400> 47  
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tatggaatgc tcggaacctt aactgaagag catgacagta ttgaggagga tgaagaagag 180  
gaagaagatg gagataaacc taaaagaaga ggtcccaaga aaaagaagat gactaaagct 240  
cgccctgaaa gattcagggc tcgaagagtc aaggccaatg ctagagaacg gacccggatg 300  
catggcctga atgatgcctt ggataatctt aggagagtca tgccatgtta ctctaaaact 360  
caaaagcttt ccaagataga gactcttcga ctggcaagga actacatctg ggccttgtct 420  
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agcttcaact atcagtctcc agggctcccc agccctcctt atggccatat ggaaacacat 660  
tctctccatc tcaagcctca accatttaag agtttgggtg actcttttgg gagccatcca 720  
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cattatacct ctgcaagtct aagttcaggg catgtgcatt caactccctt tcagactggc 900  
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<210> 48  
 <211> 330  
 <212> PRT  
 <213> Mus musculus

<400> 48

Met Ala Lys Met Tyr Met Lys Ser Lys Asp Met Val Glu Leu Val Asn  
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Thr Gln Ser Trp Met Asp Lys Gly Leu Ser Ser Gln Asn Glu Met Lys  
 20 25 30

Glu Gln Glu Arg Arg Pro Gly Ser Tyr Gly Met Leu Gly Thr Leu Thr  
 35 40 45

Glu Glu His Asp Ser Ile Glu Glu Asp Glu Glu Glu Glu Glu Asp Gly  
 50 55 60

Asp Lys Pro Lys Arg Arg Gly Pro Lys Lys Lys Lys Met Thr Lys Ala  
 65 70 75 80

Arg Leu Glu Arg Phe Arg Ala Arg Arg Val Lys Ala Asn Ala Arg Glu  
 85 90 95

Arg Thr Arg Met His Gly Leu Asn Asp Ala Leu Asp Asn Leu Arg Arg  
 100 105 110

Val Met Pro Cys Tyr Ser Lys Thr Gln Lys Leu Ser Lys Ile Glu Thr  
 115 120 125

Leu Arg Leu Ala Arg Asn Tyr Ile Trp Ala Leu Ser Glu Val Leu Glu  
 130 135 140

Thr Gly Gln Thr Leu Glu Gly Lys Gly Phe Val Glu Met Leu Cys Lys  
 145 150 155 160

Gly Leu Ser Gln Pro Thr Ser Asn Leu Val Ala Gly Cys Leu Gln Leu  
 165 170 175

Gly Pro Gln Ser Thr Leu Leu Glu Lys His Glu Glu Lys Ser Ser Ile  
 180 185 190

Cys Asp Ser Thr Ile Ser Val His Ser Phe Asn Tyr Gln Ser Pro Gly  
195 200 205

Leu Pro Ser Pro Pro Tyr Gly His Met Glu Thr His Ser Leu His Leu  
210 215 220

Lys Pro Gln Pro Phe Lys Ser Leu Gly Asp Ser Phe Gly Ser His Pro  
225 230 235 240

Pro Asp Cys Ser Thr Pro Pro Tyr Glu Gly Pro Leu Thr Pro Pro Leu  
245 250 255

Ser Ile Ser Gly Asn Phe Ser Leu Lys Gln Asp Gly Ser Pro Asp Leu  
260 265 270

Glu Lys Ser Tyr Asn Phe Met Pro His Tyr Thr Ser Ala Ser Leu Ser  
275 280 285

Ser Gly His Val His Ser Thr Pro Phe Gln Thr Gly Thr Pro Arg Tyr  
290 295 300

Asp Val Pro Val Asp Leu Ser Tyr Asp Ser Tyr Ser His His Ser Ile  
305 310 315 320

Gly Thr Gln Leu Asn Thr Ile Phe Ser Asp  
325 330

<210> 49  
<211> 2264  
<212> DNA  
<213> FROG

<400> 49  
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aaaaactttc caagtatgag actctacaga tggcactgag ctacatcatg gcactaagca 480  
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cagcaggcaa ggtactatag acctgaagat agcagtgtat tcctacacac agcagccaat	720
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<210> 50

<211> 138  
 <212> PRT  
 <213> FROG

<400> 50

Met Lys Ser Asp Ser Pro Val His Gly Glu Ser His Thr Glu Cys Gln  
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Ser Pro Cys Pro Leu Ser Cys Met Pro Ala Arg Leu Glu Gly Ser Thr  
 20 25 30

Lys Arg Arg Leu Ala Ala Asn Ala Arg Glu Arg Arg Arg Met Gln Gly  
 35 40 45

Leu Asn Thr Ala Phe Asp Ser Leu Arg Lys Val Val Pro Gln Trp Gly  
 50 55 60

Glu Asp Lys Lys Leu Ser Lys Tyr Glu Thr Leu Gln Met Ala Leu Ser  
 65 70 75 80

Tyr Ile Met Ala Leu Ser Arg Ile Leu Thr Glu Ala Glu Arg Tyr Ser  
 85 90 95

Arg Thr Asp Pro Gly Glu Trp Thr Lys Met His Phe Asp His Ile Gln  
 100 105 110

Glu Glu Gln Cys Leu Ser Tyr Met Gly Val Arg Cys Pro Arg Asp Cys  
 115 120 125

Asp Arg Tyr Leu Pro Gln Thr Phe Ser His  
 130 135

<210> 51  
 <211> 2123  
 <212> DNA  
 <213> FROG

<400> 51

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 ccttcgatag tctgaggaaa gttgtaccac aatgggggtga agacaaacaa ctttccaaat 420

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gacttacctg	tacataatcc	ctatgaaacc	aagacaatgt	gtggggaata	agaggatttg	1980
ctgcacaaat	tagggcagag	atacatgggc	tgactgtgac	aaatctcctc	ttcttcggag	2040
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cctaacgagg	caacttcagc	acg				2123

<210> 52



<211> 138  
<212> PRT  
<213> FROG

<400> 52

Met Lys Ser Asp Ser Pro Val His Arg Glu Ser His Thr Gly Cys Gln  
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Ser Pro Cys Pro Leu Arg Cys Leu Pro Ala Arg Leu Glu Gly Ser Thr  
20 25 30

Lys Arg Arg Leu Ala Ala Asn Ala Arg Glu Arg Arg Arg Met Gln Gly  
35 40 45

Leu Asn Thr Ala Phe Asp Ser Leu Arg Lys Val Val Pro Gln Trp Gly  
50 55 60

Glu Asp Lys Gln Leu Ser Lys Tyr Glu Thr Leu Gln Met Ala Leu Ser  
65 70 75 80

Tyr Ile Met Ala Leu Ser Arg Ile Leu Ser Glu Ala Glu Arg Tyr Ser  
85 90 95

Arg Thr Asp Pro Glu Glu Trp Thr Asn Ile Gln Tyr Asp His Ile Glu  
100 105 110

Glu Glu Gln Cys Leu Ser Tyr Met Glu Val Arg Cys Pro Arg Asp Cys  
115 120 125

Asp Arg Tyr Leu Pro Gln Thr Phe Ser His  
130 135

<210> 53  
<211> 136  
<212> DNA  
<213> BEETLE

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atggcccaga cctaca 136

<210> 54  
<211> 45  
<212> PRT  
<213> BEETLE

<400> 54

Ala Ala Asn Ala Arg Glu Arg Arg Arg Met Asn Gly Leu Asn Glu Ala  
 1 5 10 15

Phe Asp Arg Leu Arg Gln Val Ile Pro Ser Leu Asp Ala Asp His Lys  
 20 25 30

Leu Ser Lys Phe Glu Thr Leu Gln Met Ala Gln Thr Tyr  
 35 40 45

<210> 55  
 <211> 137  
 <212> DNA  
 <213> BEETLE

<400> 55  
 gcggcgcaatg cgagggagag gcggaggatg aacagtttga atgacgcctt cgacaggctg 60  
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 atggccccaga cctacat 137

<210> 56  
 <211> 45  
 <212> PRT  
 <213> BEETLE

<400> 56

Ala Ala Asn Ala Arg Glu Arg Arg Arg Met Asn Ser Leu Asn Asp Ala  
 1 5 10 15

Phe Asp Arg Leu Arg Asp Val Val Pro Ser Leu Gly Asn Asp Arg Lys  
 20 25 30

Leu Ser Lys Phe Glu Thr Leu Gln Met Ala Gln Thr Tyr  
 35 40 45

<210> 57  
 <211> 1572  
 <212> DNA  
 <213> HUMAN

<220>  
 <221> misc\_feature  
 <222> (1497)..(1564)  
 <223> n can be any nucleotide

<400> 57  
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 gcgcctgccc gcgccctcca ttggctgaga agacacgcga ccggcgcgag gaggggggtg 120

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ggagaggagc ggggggagac tgagtggcgc gtgccgcttt ttaaaggggc gcagcgcctt 180
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agggtcgagg agggaaaaaa aaataagacg ttgcagaaga gacccggaag gggccttttt 300
tttggttgag ctggtgtccc agtgctgcct ccgatcctga gcgtccgagc ctttgagtg 360
caatgtcccc cctgctgcat gcagaagagt gggctgaagt gaaggagttg ggagaccacc 420
atcgccagcc ccagccgcat catctcccgc aaccgccgcc gccgccgcag ccacctgcaa 480
ctttgcaggc gagagagcat cccgtctacc cgctgagct gtccctcctg gacagcaccg 540
accacgcgc ctggctggct cccactttgc agggcatctg cacggcacgc gccgcccagt 600
atttgctaca ttccccggag ctgggtgcct cagaggccgc tgcgccccgg gacgaggtgg 660
acggccgggg ggagctggta aggaggagca gcggcgggtgc cagcagcagc aagagccccg 720
ggccggtgaa agtgccggaa cagctgtgca agctgaaagg cggggtgggtg gtagacgagc 780
tgggctgcag ccgccaacgg gcccttcca gcaaacagggt gaatggggtg cagaagcaga 840
gacggctagc agccaacgcc agggagcggc gcaggatgca tgggctgaac cacgccttcg 900
accagctgcg caatgttatc ccgtcgttca acaacgacaa gaagctgtcc aaatatgaga 960
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ccgcggcctc ctatgaaggg ggcgcgggca acgcgaccgc agctggggct cagcaggctt 1140
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cttctgcggg agggactcgc gtgcagctgg acgctctgca cttctcgact ttcgaggaca 1260
gcgccctgac agcgatgatg gcgcaaaaga atttgtctcc ttctctcccc gggagcatct 1320
tgcagccagt gcaggaggaa aacagcaaaa cttcgectcg gtccacaga agcgacgggg 1380
aattttcccc ccattcccat tacagtgact cggatgaggc aagttaggaa ggtgacagaa 1440
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gctncagatg gt 1572

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<210> 58
<211> 354
<212> PRT
<213> HUMAN

<400> 58

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Met Ser Arg Leu Leu His Ala Glu Glu Trp Ala Glu Val Lys Glu Leu
1           5           10           15

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Gly Asp His His Arg Gln Pro Gln Pro His His Leu Pro Gln Pro Pro  
 20 25 30

Pro Pro Pro Gln Pro Pro Ala Thr Leu Gln Ala Arg Glu His Pro Val  
 35 40 45

Tyr Pro Pro Glu Leu Ser Leu Leu Asp Ser Thr Asp Pro Arg Ala Trp  
 50 55 60

Leu Ala Pro Thr Leu Gln Gly Ile Cys Thr Ala Arg Ala Ala Gln Tyr  
 65 70 75 80

Leu Leu His Ser Pro Glu Leu Gly Ala Ser Glu Ala Ala Ala Pro Arg  
 85 90 95

Asp Glu Val Asp Gly Arg Gly Glu Leu Val Arg Arg Ser Ser Gly Gly  
 100 105 110

Ala Ser Ser Ser Lys Ser Pro Gly Pro Val Lys Val Arg Glu Gln Leu  
 115 120 125

Cys Lys Leu Lys Gly Gly Val Val Val Asp Glu Leu Gly Cys Ser Arg  
 130 135 140

Gln Arg Ala Pro Ser Ser Lys Gln Val Asn Gly Val Gln Lys Gln Arg  
 145 150 155 160

Arg Leu Ala Ala Asn Ala Arg Glu Arg Arg Arg Met His Gly Leu Asn  
 165 170 175

His Ala Phe Asp Gln Leu Arg Asn Val Ile Pro Ser Phe Asn Asn Asp  
 180 185 190

Lys Lys Leu Ser Lys Tyr Glu Thr Leu Gln Met Ala Gln Ile Tyr Ile  
 195 200 205

Asn Ala Leu Ser Glu Leu Leu Gln Thr Pro Ser Gly Gly Glu Gln Pro  
 210 215 220

Pro Pro Pro Pro Ala Ser Cys Lys Ser Asp His His His Leu Arg Thr  
 225 230 235 240

Ala Ala Ser Tyr Glu Gly Gly Ala Gly Asn Ala Thr Ala Ala Gly Ala  
 245 250 255

Gln Gln Ala Ser Gly Gly Ser Gln Arg Pro Thr Pro Pro Gly Ser Cys  
 260 265 270

Arg Thr Arg Phe Ser Ala Pro Ala Ser Ala Gly Gly Tyr Ser Val Gln  
 275 280 285

Leu Asp Ala Leu His Phe Ser Thr Phe Glu Asp Ser Ala Leu Thr Ala  
 290 295 300

Met Met Ala Gln Lys Asn Leu Ser Pro Ser Leu Pro Gly Ser Ile Leu  
 305 310 315 320

Gln Pro Val Gln Glu Glu Asn Ser Lys Thr Ser Pro Arg Ser His Arg  
 325 330 335

Ser Asp Gly Glu Phe Ser Pro His Ser His Tyr Ser Asp Ser Asp Glu  
 340 345 350

Ala Ser

<210> 59  
 <211> 485  
 <212> DNA  
 <213> CHICKEN

<220>  
 <221> misc\_feature  
 <222> (147)..(147)  
 <223> n can be any nucleotide

<400> 59  
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 aggcggcccc tggcgggggg cgcggcncgc gttccggcgg gagcagcccc gggggagcgc 180  
 ggggcggcgg cgggcgcgcg gggcggcggc ggcggggccg ggccgcgggc gcaggtgagc 240  
 ggcgtgcaga agcagcggcg gctggcggcc aacgcgcggg agcggcggcg gatgcacggg 300  
 ctgaaccacg ccttcgacca gctgcgtaat gtcatcccct ccttcaacaa cgacaagaag 360  
 ctctccaagt acgagacgct gcagatggcg caaatctaca tcagcgcctt cgccgagctg 420  
 ctgcacgggg cgcgcgcgcc ccccgagccg cccgccaagg ccgagctccg cggggccccc 480  
 ttcca 485

<210> 60  
 <211> 161

<212> PRT  
 <213> CHICKEN

<400> 60

Pro Leu Leu Gly Pro Asp Gly Ala Ala Ala Ser Pro Pro Ala Gly  
 1 5 10 15

Trp Ala Cys Ala Ala Pro His Ala Cys Pro Pro Arg Arg Arg Ala Thr  
 20 25 30

Cys Cys Pro Pro Thr Arg Arg Thr Arg Arg Pro Val Ala Gly Gly Ala  
 35 40 45

Ala Arg Val Pro Ala Gly Ala Ala Pro Gly Glu Arg Gly Ala Ala Ala  
 50 55 60

Gly Ala Arg Gly Gly Gly Gly Gly Ala Gly Pro Arg Ala Gln Val Ser  
 65 70 75 80

Gly Val Gln Lys Gln Arg Arg Leu Ala Ala Asn Ala Arg Glu Arg Arg  
 85 90 95

Arg Met His Gly Leu Asn His Ala Phe Asp Gln Leu Arg Asn Val Ile  
 100 105 110

Pro Ser Phe Asn Asn Asp Lys Lys Leu Ser Lys Tyr Glu Thr Leu Gln  
 115 120 125

Met Ala Gln Ile Tyr Ile Ser Ala Leu Ala Glu Leu Leu His Gly Pro  
 130 135 140

Pro Ala Pro Pro Glu Pro Pro Ala Lys Ala Glu Leu Arg Gly Ala Pro  
 145 150 155 160

Phe

<210> 61  
 <211> 138  
 <212> DNA  
 <213> PUFFER FISH

<400> 61

gcggcgaacg cgaggagag gaggagaatg cacggcctga ataaagcggtt tgacgaactg 60  
 aggagcggtca ttccttcctt ggaaaatgag agaaagctct ccaagtatga cactctccag 120  
 atggcccaaaa cctacatc 138

<210> 62  
 <211> 46  
 <212> PRT  
 <213> PUFFER FISH

<400> 62

Ala Ala Asn Ala Arg Glu Arg Arg Arg Met His Gly Leu Asn Lys Ala  
 1 5 10 15

Phe Asp Glu Leu Arg Ser Val Ile Pro Ser Leu Glu Asn Glu Arg Lys  
 20 25 30

Leu Ser Lys Tyr Asp Thr Leu Gln Met Ala Gln Thr Tyr Ile  
 35 40 45

<210> 63  
 <211> 1477  
 <212> DNA  
 <213> DROSOPHILA

<400> 63

atcatcttgt tagcggcttt agagccgaat cgttttctag cgccatttta agctcgcaac	60
gaactgaggt ataaccgggc tctctgagac cgctgcaact caccaccaac tgccattggt	120
cgtgccactc gggcggcacg tgctgccttc tgtggcaact cgtttacctg cccccctacc	180
tgcctttcag gcccttctga ccgtcgtggt ggatttgtga gtataaatag ggccgaaagg	240
acgagagacc agtcagaaac ccgccagcac tcgcagcgtt cgtatcgttt catccagcaa	300
cataacacca ccatacagca gcagcaacat gtcgtccagt gagatctatc gctactacta	360
caagacctcc gaggacttgc agggcttcaa gacagccgcc gccgagccgt acttcaatcc	420
catggcagcc tacaatcccg gcgtgaccca ctaccagttc aatggcaaca ccctggccag	480
cagcagcaac tacttgctcg ccaatggctt catcagcttc gagcaggcca gttccgatgg	540
ctggatctcc tctcgcggg ctagccaccg atctgagagt cccgagtatg tggatctcaa	600
taccatgtac aatggaggct gcaacaacat ggcccagaac caacaatacg gaatgattat	660
ggagcagtct gttgtttcca cagcgctgc aattccagtg gcctctctc cggcagtgga	720
ggatcatgggc tctccaacg tgggcacttg caaaacgatt ccagcctcag cagctccgaa	780
accgaagcgt agctatacca agaagaacca gccaaagcacc accgccacct ccacaccgac	840
tgcagctgcg gagtcatctg cctcagtga tctctacacg gaggagtcc agaactttga	900
ctttgacaac tccgccttgt tcgatgacag cgctgaggat gacgaggacc tcatgctctt	960
cagtggcggt gaggacttcg atggcaatga tggatccttt gacttggccg atggtgagaa	1020
ccaagatgcc gctgccggag gctctggaaa gaagaggcgt ggcaagcaga tcacaccgct	1080

cgtgaagagg aagcgtcgcc tggccgcca tgcacgtgag cgtcgtcgga tgcagaacct 1140  
 caaccaggcc ttcgatcgtc tccgccagta ccttccctgt ctgggaaacg atcgccagct 1200  
 gtccaaacac gagaccctcc aaatggccca gacctacata tccgctctcg gggatctgct 1260  
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 taaggaagac aaaataaaag caccattaat aatttaa 1477

<210> 64  
 <211> 312  
 <212> PRT  
 <213> DROSOPHILA

<400> 64

Met Ser Ser Ser Glu Ile Tyr Arg Tyr Tyr Tyr Lys Thr Ser Glu Asp  
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Leu Gln Gly Phe Lys Thr Ala Ala Ala Glu Pro Tyr Phe Asn Pro Met  
 20 25 30

Ala Ala Tyr Asn Pro Gly Val Thr His Tyr Gln Phe Asn Gly Asn Thr  
 35 40 45

Leu Ala Ser Ser Ser Asn Tyr Leu Ser Ala Asn Gly Phe Ile Ser Phe  
 50 55 60

Glu Gln Ala Ser Ser Asp Gly Trp Ile Ser Ser Ser Pro Ala Ser His  
 65 70 75 80

Arg Ser Glu Ser Pro Glu Tyr Val Asp Leu Asn Thr Met Tyr Asn Gly  
 85 90 95

Gly Cys Asn Asn Met Ala Gln Asn Gln Gln Tyr Gly Met Ile Met Glu  
 100 105 110

Gln Ser Val Val Ser Thr Ala Pro Ala Ile Pro Val Ala Ser Pro Pro  
 115 120 125

Ala Val Glu Val Met Gly Ser Ser Asn Val Gly Thr Cys Lys Thr Ile  
 130 135 140

Pro Ala Ser Ala Ala Pro Lys Pro Lys Arg Ser Tyr Thr Lys Lys Asn  
 145 150 155 160



Gln Pro Ser Thr Thr Ala Thr Ser Thr Pro Thr Ala Ala Ala Glu Ser  
165 170 175

Ser Ala Ser Val Asn Leu Tyr Thr Glu Glu Phe Gln Asn Phe Asp Phe  
180 185 190

Asp Asn Ser Ala Leu Phe Asp Asp Ser Val Glu Asp Asp Glu Asp Leu  
195 200 205

Met Leu Phe Ser Gly Gly Glu Asp Phe Asp Gly Asn Asp Gly Ser Phe  
210 215 220

Asp Leu Ala Asp Gly Glu Asn Gln Asp Ala Ala Ala Gly Gly Ser Gly  
225 230 235 240

Lys Lys Arg Arg Gly Lys Gln Ile Thr Pro Val Val Lys Arg Lys Arg  
245 250 255

Arg Leu Ala Ala Asn Ala Arg Glu Arg Arg Arg Met Gln Asn Leu Asn  
260 265 270

Gln Ala Phe Asp Arg Leu Arg Gln Tyr Leu Pro Cys Leu Gly Asn Asp  
275 280 285

Arg Gln Leu Ser Lys His Glu Thr Leu Gln Met Ala Gln Thr Tyr Ile  
290 295 300

Ser Ala Leu Gly Asp Leu Leu Arg  
305 310

<210> 65  
<211> 907  
<212> DNA  
<213> FROG

<400> 65  
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ctgctacacg gcgctgctac tgccgctgac tgggtgcgagc tgaaggagct tccatccgag 120  
gccggggtct tggccagaga ttacctacta gacagcagcg acccccgcgc ctggctctcc 180  
gccacttccc tgcaaagtcg ccctgagtac gtgctgcacc ccccgggccg ggccggggcg 240  
acaaggtgcg ggaactgtgc aaactgaagg ggctgcggga tgatgatgat gatgaggagg 300  
atgatgagga ggaggaagag agatccgagg ggctgtgcag acacaggggt cccctgggca 360  
agggccctgg tggggttcag aagcagagga gactggcagc caatgccagg gagaggagga 420

ggatgcacgg gctcaatcat gccttcgatc agctccgtaa tgtcatccct tccttcaata 480  
 acgacaagaa actctccaaa tacgagaccc tgcagatggc tcagatctac atcaacgccc 540  
 tgtccgacct gctgcaggcg cccccgact ccagagatcc cccctgcccg cccacctacc 600  
 aactgcattc ggggccagag cccagggttag tccagtctgg cagcatgaga ttctcggaga 660  
 cttccccccg acagtcccc ctcagccaat tccaggaggg agctgctccc agaaggggaat 720  
 aggatctggg cccatcttca tcttctcggg aagacatcgc ccatcttcat cttcggggag 780  
 aagacagcaa gacatcgcaa gatctcatcg gagtgacggc gaattccggt ctccctatag 840  
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 aggcggt 907

<210> 66  
 <211> 259  
 <212> PRT  
 <213> FROG

<400> 66

Met Ala Arg Leu Leu His Gly Ala Ala Thr Ala Ala Asp Trp Cys Glu  
 1 5 10 15

Leu Lys Glu Leu Pro Ser Glu Ala Gly Leu Leu Ala Arg Asp Tyr Leu  
 20 25 30

Leu Asp Ser Ser Asp Pro Arg Ala Trp Leu Ser Ala Thr Ser Leu Gln  
 35 40 45

Ser Arg Pro Glu Tyr Val Leu His Pro Pro Gly Arg Ala His Lys Val  
 50 55 60

Arg Glu Leu Cys Lys Leu Lys Gly Leu Arg Asp Asp Asp Asp Asp Glu  
 65 70 75 80

Glu Glu Asp Asp Glu Glu Glu Glu Glu Arg Ser Glu Gly Leu Cys Arg  
 85 90 95

His Arg Gly Pro Pro Gly Lys Gly Pro Gly Gly Val Gln Lys Gln Arg  
 100 105 110

Arg Leu Ala Ala Asn Ala Arg Glu Arg Arg Arg Met His Gly Leu Asn  
 115 120 125

His Ala Phe Asp Gln Leu Arg Asn Val Ile Pro Ser Phe Asn Asn Asp  
 130 135 140

Lys Lys Leu Ser Lys Tyr Glu Thr Leu Gln Met Ala Gln Ile Tyr Ile  
 145 150 155 160

Asn Ala Leu Ser Asp Leu Leu Gln Ala Pro Pro Asp Ser Arg Asp Pro  
 165 170 175

Pro Cys Pro Pro Thr Tyr Gln Leu His Ser Gly Pro Glu Pro Arg Leu  
 180 185 190

Val Gln Ser Gly Ser Cys Met Arg Phe Ser Gly Asp Phe Pro Gly Gln  
 195 200 205

Ser Pro Leu Ser Phe Gln Phe Gln Glu Gly Ala Ala Leu Ser Gly Lys  
 210 215 220

Gly Ile Gly Ser Ala Pro Ser Ser Ser Ser Gly Glu Asp Ser Lys Thr  
 225 230 235 240

Ser Pro Arg Ser His Arg Ser Asp Gly Glu Phe Arg Ser Pro Tyr Ser  
 245 250 255

Glu Ser Tyr

<210> 67  
 <211> 19  
 <212> DNA  
 <213> SYNTHETIC CONSTRUCT

<400> 67  
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<210> 68  
 <211> 19  
 <212> DNA  
 <213> SYNTHETIC CONSTRUCT

<400> 68  
 ccgctgccaa attcttttg 19

<210> 69  
 <211> 37  
 <212> DNA  
 <213> HUMAN

<400> 69  
 gggggcactg acagtaatgc atgccgtatt cgaagtt 37

<210> 70  
<211> 21  
<212> PRT  
<213> HUMAN

<400> 70

Ala Ala Asn Ala Arg Glu Arg Arg Arg Met His Gly Leu Asn His Ala  
1 5 10 15

Phe Asp Gln Leu Arg  
20